

Qy 181 KEEDNRDPQOREYEDCRRCEQQPQQYOCORCRCREOQRQHGGGLDLINPQRCGSGRY 240
 Db 181 KEEDNRDPQOREYEDCRRCEQQPQQYOCORCRCREOQRQHGGGLDLINPQRCGSGRY 240
 Qy 241 EGEEKOSDNYYFEDERSLSSTRFRTEEGHSYLENYGRSKLRLALKNYRLVLFANPA 300
 Db 241 EGEEKOSDNYYFEDERSLSSTRFRTEEGHSYLENYGRSKLRLALKNYRLVLFANPA 300
 Qy 301 FVLPTHLDADAILLYGGRGALKMHRDNRBESYNLECGDVRIPAGTTFYLINRNNRL 360
 Db 301 FVLPTHLDADAILLYGGRGALKMHRDNRBESYNLECGDVRIPAGTTFYLINRNNRL 360
 Qy 361 HIAKFLQTISPGQYKEFPAGQNPENPLSTESKEILEALNTAQERLNGVLGQREGV 420
 Db 361 HIAKFLQTISPGQYKEFPAGQNPENPLSTFSKILEALNTAQERLNGVLGQREGV 420
 Qy 421 IISASQEQLRLTRDSESRRWHTRRGESSRGPQNLNKRPLYSNKYGOAYEVKPEDYR 480
 Db 421 IISASQEQLRLTRDSESRRWHTRRGESSRGPQNLNKRPLYSNKYGOAYEVKPEDYR 480
 Qy 481 OLQDMQSVFANTITQGSMGPMFFENRSTKVVVVAASGEADVEMACPHLSRHHGGGKR 540
 Db 481 OLQDMQSVFANTITQGSMGPMFFENRSTKVVVVAASGEADVEMACPHLSRHHGGGKR 540
 Qy 541 HEEEDVHYEQYKARLSKREAVWVGHPVVFVSSGENNLLEAFGINAONNHENFLAGR 600
 Db 541 HEEEDVHYEQYKARLSKREAVWVGHPVVFVSSGENNLLEAFGINAONNHENFLAGR 600
 Qy 601 ERNVLOQIEPQAMELAAFAARKEVKEVLFNSQDESFFPGQRHQHOOQSRSRKQQPLVSI 660
 Db 601 ERNVLOQIEPQAMELAAFAARKEVKEVLFNSQDESFFPGQRHQHOOQSRSRKQQPLVSI 660
 Qy 661 LDFVGF 666
 Db 661 LDFVGF 666

RESULT 2
 Q9SP15 PRELIMINARY; PRT; 666 AA.
 ID Q9SP15
 AC 09SP15;
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VICTILIN PRECURSOR.
 GN AMP2.

Macadamia interifolia (Macadamia nut).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
 NCBI_TaxID=6098;
 [1]
 SEQUENCE FROM N.A.

TISSUE=NUT KERNEL;
 RA Marcus J.P., Goult K.C., Green J.L., Manners J.M.;
 RT "A family of antimicrobial peptides is produced by processing of a 7S
 globulin protein in Macadamia integrifolia kernels.";
 RL Plant J. 0:0-0(1999);
 EMBL: AF161883; AA|54|244.1; -.
 DR HSSP: P02853; 2PBL.
 DR INTERPRO; IPR00113; -.
 DR PF00546; Seedstore_7s; 1.
 SEQUENCE 666 AA; 78217 MW; C752B84B2DF0224 CRC64;

Query Match 96.6%; Score 3412; DB 10; Length 666;
 Best Local Similarity 96.1%; Pred. No. 1e-239; Indels 0; Gaps 0;
 Matches 640; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MAINTNSLCSLFLSLFLSLFLSTVSLAESFDROTEYECKROCMOLETSQMRRCVQSCD 60
 Db 1 MAINTNSLCSLFLSLFLSLFLSTVSLAESFDROTEYECKROCMOLETSQMRRCVQSCD 60

Qy 61 KFEEEDIDWSYDNDQDPQDCQDCQESPRODYCQRCKECEEEVNR 120
 Db 61 KFEEEDIDWSYDNDQDPQDCQDCQESPRODYCQRCKECEEEVNR 120
 Qy 121 DPQQYEQCQRCQRCRTEPFRHMQTCQRCRERRYKEKRCQKREQDREDEYERM 180
 Db 121 DPQQYEQCQRCQRCRTEPFRHMQTCQRCRERRYKEKRCQKREQDREDEYERM 180
 Qy 181 FEEDNRDPQOREYEDCRRCEQQPQQYOCORCRCREOQRQHGGGLDLINPQRCGSGRY 240
 Db 181 FEEDNRDPQOREYEDCRRCEQQPQQYOCORCRCREOQRQHGGGLDLINPQRCGSGRY 240
 Qy 241 EGEEKOSDNYYFEDERSLSSTRFRTEEGHSYLENYGRSKLRLALKNYRLVLFANPA 300
 Db 241 EGEEKOSDNYYFEDERSLSSTRFRTEEGHSYLENYGRSKLRLALKNYRLVLFANPA 300
 Qy 301 FVLPTHLDADAILLYGGRGALKMHRDNRBESYNLECGDVRIPAGTTFYLINRNNRL 360
 Db 301 FVLPTHLDADAILLYGGRGALKMHRDNRBESYNLECGDVRIPAGTTFYLINRNNRL 360
 Qy 361 HIAKFLQTISPGQYKEFPAGQNPENPLSTESKEILEALNTAQERLNGVLGQREGV 420
 Db 361 HIAKFLQTISPGQYKEFPAGQNPENPLSTFSKILEALNTAQERLNGVLGQREGV 420
 Qy 421 IISASQEQLRLTRDSESRRWHTRRGESSRGPQNLNKRPLYSNKYGOAYEVKPEDYR 480
 Db 421 IISASQEQLRLTRDSESRRWHTRRGESSRGPQNLNKRPLYSNKYGOAYEVKPEDYR 480
 Qy 481 OLQDMQSVFANTITQGSMGPMFFENRSTKVVVVAASGEADVEMACPHLSRHHGGGKR 540
 Db 481 OLQDMQSVFANTITQGSMGPMFFENRSTKVVVVAASGEADVEMACPHLSRHHGGGKR 540
 Qy 541 HEEEDVHYEQYKARLSKREAVWVGHPVVFVSSGENNLLEAFGINAONNHENFLAGR 600
 Db 541 HEEEDVHYEQYKARLSKREAVWVGHPVVFVSSGENNLLEAFGINAONNHENFLAGR 600
 Qy 601 ERNVLOQIEPQAMELAAFAARKEVKEVLFNSQDESFFPGQRHQHOOQSRSRKQQPLVSI 660
 Db 601 ERNVLOQIEPQAMELAAFAARKEVKEVLFNSQDESFFPGQRHQHOOQSRSRKQQPLVSI 660
 Qy 661 LDFVGF 666
 Db 661 LDFVGF 666

RESULT 3
 Q9SP13 PRELIMINARY; PRT; 625 AA.
 ID Q9SP13
 AC 09SP13;
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VICTILIN PRECURSOR (FRAGMENT).
 GN AMP2.

Macadamia interifolia (Macadamia nut).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
 NCBI_TaxID=6098;
 [1]
 SEQUENCE FROM N.A.

TISSUE=NUT KERNEL;
 RA Marcus J.P., Goult K.C., Green J.L., Manners J.M.;
 RT "A family of antimicrobial peptides is produced by processing of a 7S
 globulin protein in Macadamia integrifolia.";
 RL Plant J. 0:0-0(1999);
 EMBL: AF161885; AA|54|246.1; -.
 DR HSSP; P02853; 2PBL.
 DR INTERPRO; IPR00113; -.
 DR PF00546; Seedstore_7s; 1.
 FT NON_TER 1
 SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;

RESULT	4	DR	PFAM: PF00546; Seedstore_7s; 1.
ID	Q9SEW4	FT	NON_TER 1
AC	Q9SEW4:	SEQUENCE	593 AA; 9BA127E19B18C0D8 CRC64;
DT	01-MAY-2000 (TREMBLrel. 13, Created)	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
DE	VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
OS	Juglans regia (English walnut).	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
OC	Magnoliophyta; eudicots; Rosidae; eurosids I; RGALES; Juglandaceae; Juglans.	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
OC	NCBI_TaxID=51240;	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
RN	[1]	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
RP	SEQUENCE FROM N.A. TISSUE=SOMATIC EMBRYO LINE;	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
RC	STRAIN=CV; SUNLAND.	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
RA	Teuber, S.S., Jarvis, K.C., Peterson, W.R., Dandekar, A.M., Ansari, A.A.;	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
RT	Identification and cloning of a cDNA encoding a vicilin-like protein, Jug r 2, from English walnut kernel (Juglans regia); a major food allergen.;	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
DR	HSSP: P02853; 2PHL.	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
DR	INTERPRO; IPR00113; -.	Q9SEW4:	Query Match 91.0%; Score 3215; DB 10; Length 625; Best Local Similarity 96.6%; Pred. No. 1..9e-225; Matches 604; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
RESULT	5	DR	PFAM: PF00546; Seedstore_7s; 1.
ID	Q9ZWI3	FT	NON_TER 1
AC	Q9ZWI3:	SEQUENCE	810 AA; 9BA127E19B18C0D8 CRC64;
DT	01-MAY-1999 (TREMBLrel. 10, Created)	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
DT	01-OCT-1999 (TREMBLrel. 10, Last sequence update)	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
DE	RGALES; Juglandaceae; Juglans.	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
OS	Juglans regia (English walnut).	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
OC	Magnoliophyta; eudicots; Rosidae; eurosids I; RGALES; Juglandaceae; Juglans.	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
OC	NCBI_TaxID=3661;	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
RN	[1]	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
RP	SEQUENCE FROM N.A.	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
RC	STRAIN=KUROKAWA; AMAKURI NANKIN; TISSUE=CYTOLEBON;	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
RA	Yamada, K., Shimada, T., Kondo, M., Nishimura, M., Hara-Nishimura, I.;	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;
RT	"Multiple functional proteins are produced by cleaving Nsn-Gln bonds	Q9ZWI3:	Query Match 37.5%; Score 1324.5; DB 10; Length 593; Best Local Similarity 44.3%; Pred. No. 3..8e-83; Matches 274; Conservative 118; Mismatches 169; Indels 57; Gaps 16;

RESULT	7	RESULT	8
Q03865	PRELIMINARY;	Q03678	PRELIMINARY;
ID	Q03865;	ID	Q03678;
AC	003865;	AC	003678;
DT	01-NOV-1996 (TREMBLrel. 01, Created)	DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-2000 (TREMBLrel. 15, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	VICILIN-LIKE EMBRYO STORAGE PROTEIN.	DE	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
GN	GB31-L.	GN	FETAL STORAGE PROTEIN.
OS	Zea mays (Maize).	OS	BEG1 OR GB31.
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.	OC	Hordeum vulgare (Barley), and Triticum aestivum (wheat).
OX	NCBI_TaxID=4577;	OX	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
RN	[1]	RN	NCBI_TaxID=4513, 4565;
RP	SEQUENCE FROM N.A.	RP	[1]
RC	STRAIN=W64A;	RC	SEQUENCE FROM N.A.
RX	MEDLINE=922090707; PubMed=1752424;	RX	MEDLINE=93287983; PubMed=8510647;
RA	Belanger F.C., Kitz A.L.;	RA	Heck G.R., Chamberlain A.C., Ho T.H.D.;
RT	"Molecular basis for allelic polymorphism of the maize Globulin-1 gene.";	RT	"Barley embryo globulin 1 gene, Bieg: characterization of cDNA, chromosome mapping and regulation of expression.";
RL	Genetics 129:863-872(1991).	RL	Mol. Genet. 239:209-218(1993).
EMBL	x59083; CA441809.1; -.	EMBL	M64372; AA32936.1; -.
PR	HESP; P50477; 1CAU.	PR	EMBL; M81719; AA34269.1; -.
DR	MENDEL; 11234; Zearna;1188;11234.	DR	HSSP; P02853; 2PHL.
DR	INTERPRO; IPR000901; -.	DR	MENDEL; 8553; Horvai;1188;8553.
DR	PFAM; PF00546; Seedstore_7s; 1.	DR	INTERPRO; IPR001113; -.
DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.	DR	PFAM; PF00546; Seedstore_7s; 1.
DR	PRODOM; PD001059; -; 1.	DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
KW	Seed storage protein.	KW	PRODOM; PD081059; -; 1.
SQ	SEQUENCE 582 AA; 66162 MW; 680B5FEC07CB885 CRC64;	SQ	SEQUENCE 637 AA; 72252 MW; F323F4FF99947C3C CRC64;
Query Match	25.3%; Score 895; DB 10; Length 582;	Query Match	24.8%; Score 875; DB 10; Length 637;
Best Local Similarity	39.6%; Pred. No. 5.8e-57;	Best Local Similarity	35.6%; Pred. No. 1.9e-55;
Matches	201; Conservative 83; Mismatches 183; Indels 40; Gaps 11;	Matches	227; Conservative 99; Mismatches 206; Indels 106; Gaps 22;
Qy	182 EEDNKRDPQREYEDCRRCEQEQPROQYQCCRRCRE----QDQHGRGQDLINPQRG 235	Qy	70 SKYDNODDPQ---TDCOCQRCRQOBGSPQQYQCCRCKEICEEEEEEYHRDQDQOYE 127
Db	25 EDDNHHHHGGHKSGCQYRCDRDPWHORPROLCREERERKQRORSRHEAD----RS 79	Db	27 ASHDDEDRRGHSLSQOCVQCRQER-PR--YSHARCYQOC----RDDQOQH- 71
Qy	236 GSG---RYEEEKQSD-NPYFEDERSLSLSTRFREPEHGSVLENFYGKRLRALKNYR 290	Qy	128 QCQERCORHETEPRHMOTCQRCRERYEKKRQKQRYEQREDEE---KYERMKE 182
Db	80 GCGSENEREQQEKEQKODRRYVFDRRSFRVRSRQSGSLRVLPEDEVSRLLRQSRDYR 139	Db	72 ----GRHEEEEOGRGRGHWGHEGEEHGRGRGGRGEGEEHGRGRGEGERE 125
Qy	291 LIVLLEAAMPNAFLYPLTHIDADATLVLVGGGRGALKMHRDNRSYNLRGGDVIRAPGTFY 350	Qy	183 EDDNKRDPQREYEDCRRCEQEQPROQYQCCRRCREQQRQIGR---GDLINPQGGSG 238
Db	140 VAWLEANPRSFVUPSHITDAHCICVYAEGBEGVWTIENGERRSYTIKOGHVFVAPAGVTY 199	Db	126 DERRGRG-----HGRHIGGE-----REERGRGRGHEGEREEECRGRG 165
Qy	351 LINRDRNRLHITAKFLOTISTPGQYKEFPAGQONPEPYLSTFSKILEAALNTQAAERLR 410	Qy	239 RYEEGE-EKQSDN- PYYFEDERSLSLSTRFREPEHGSVLENFYGSKLRLALKNYR 294
Db	200 LANTDGRKKLVITKLTISPGKEFQFGFGPGRNBESFLSSFSRSIQRAAKYKTSDRLE 259	Db	166 RRGEGEDEEGDSRSPYRPGPRSRITQSDHGRFVRLRFQDSRLLRQGRDVAIM 225
Qy	411 GYLGQ---OREGVITIASQEQRELTDDE---SRWHTRRGESGRGPYMLNFRPLYS 465	Qy	295 EANPNAEVLPHTLDADAILYVGGRGALKMHRDNRSYNLCGDVIRAPGTFYLNR 354
Db	260 RLFGRRQDKGKJLIVRATEEQTRELRRHASEGGHGPWHPLPFGE-SRGPISSLDRPSIA 318	Db	226 EYNPRAFVVFPGFTDAGVGYAOGESCVLTVENGKRSYTKEGVYLVAPGSIHLANT 285
Qy	466 NYKQAYEVKEPKEDYRQLQDMVSFVANTIQGSMGPFFNRSTKVWVVAASGEVEMAC 525	Qy	355 DNNERLHAKTQLQTISTPGQYKEFPAGQONPEPYLSTFSKILEAALNTQAAERLRVIG 414
Db	319 NQHGQLYEDARSFHDLAHDVSVSFANTAGSMSAFLNTRSKFLAYVPGNGKAYEIVC 378	Db	286 DGRRKLVIAKLIHTSVPGKF-QFL---SVKPLASLSKVRRAFKTSDSRDLRLFN 339
Qy	526 PHLGRG---GRGGKRRHEEEDYH-----YEQVKARSKREAVVPGVPHPV 571	Qy	415 QO-----REGVITASQEQRELTDDE---SRWHTRRGESGRGPYMLNFRPLYS 465
Db	379 PHRQSGQESERDKGRSSEEEESSEQQEAGQCYTIRARLSPGTAVVPGHFPV 438	Db	340 ORQQRKTRSVSIVRASEEQRELRAEAGQGQHWRPLPFGSDSRDTNLQFLQRPKIA 399
Qy	572 FVSSGNLNLFAFGTMNQHNFLAGRERNVQOQIPEQPMELLEAAPRKEVEELFNSQ 631	Qy	466 NYKQAYEVKEPKEDYRQLQDMVSFVANTIQGSMGPFFNRSTKVWVVAASGEVEMAC 525
Db	439 AVASDRSNLQIVCFEVYHADRREKVFLAGD-NVQKQLDRVAKALSPASKAEEDEVLGLS 497	Db	400 NRHGRILYEDARSFHALANQDVRVAVANLPGSMWAPLYMQLQSKLAWVIEGEBOVYC 459
Qy	632 DESSIFFGPQ---HQQSSSTSKQOQ 655	Qy	526 PHL-----SGHGGGRGKRRHEEEDYH-----VHVEQVKARSKRE 560
Db	498 REKGLPQPEESGGHREEQEEEREE 524	Qy	-----SGHGGGRGKRRHEEEDYH-----VHVEQVKARSKRE 560

Db	339	-SSEDKPFLNRLRSDPFLNSKLGKFFETTPKNPQLRDLTFLRSLVNFNEGALLPHENV 397	QY	448 GESSRGYGNLFKKRPLYSNKQGOAYEVKPEPYRQLQDMDSVFLVIANITQGSMGPENTR 507
Db	508	STKVVVVASGEADVEMACPHLSGRHGG - RRGKRMHEEVDHYEQVKA.RSKREIVV 565	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Db	398	ATIVLVLINQDANIELV-----GLKEQQEQQQEQEPEVRYRAESEQDIFV 448	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Db	566	VGHVVVFVSSGNENLLFAFGINAQNHHENFLAGRERNVQOIEPQAMELAFAAPRKEVE 625	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Db	449	AGYPVVV-NATSNLNFAGINAENNORNFLAGSDQNVTSQIPSOVQELAFPGSAQAVE 506	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Qy	626	EFLNSQDESIFPGPROHQQSRSRKQQPLVSL 661	QY	455 AVSASNLLL-GFGINAENNORNFLAGSDQNVTSQIPSOVQELAFPGSAQAVE 512
Db	507	KULKNORESYFVDAQPKKKBEGNKGKR - -GPBLSSIL 540	QY	455 AVSASNLLL-GFGINAENNORNFLAGSDQNVTSQIPSOVQELAFPGSAQAVE 512
RESULT	11		Db	513 QEHSHF--ANAEPEQGEESQRKRSPISSL 541
ID	041674	PRELIMINARY;	PRT;	545 AA.
AC	041674;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	CONVICILIN PRECURSOR.			
OS	Vicia narbonensis.			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicia.			
OC	NCBI_TaxID:3912;			
RN	[1] SEQUENCE FROM N. A.			
RC	TISSUE-COTyledon;			
RA	Koch G., Koenig S., Becker C., Horstmann C., Schlesier B.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: Z71986; CAAB6513.1; -.			
DR	HSRP: P50477; ICAU:			
DR	MENDEL: 12432; Vicia1188;12432.			
DR	INTERPRO: IPR001113; -.			
DR	PFAM: PF00546; Seedstore_7s; 1.			
DR	PRODOM: PDO81059; -; 1.			
KW	Signal; Seed storage protein.			
FT	SIGNAL 1 28	POTENTIAL.		
FT	CHAIN 29 545 AA; 62810 MW; 459A876F92F5AB7E CRC64;			
SO	SEQUENCE 545 AA; 75 GLOBULIN, CONVICILIN.			
Query Match	23.2%	score 818; DB 10; Length 545;		
Best Local Similarity	34.3%	score 818; DB 10; Length 545;		
Matches	196;	Conservative 101; Mismatches 204; Indels 70; Gaps 14;		
Oy	109	ICEEEEEYNQRQDQQYEQCQERCORHETEPHRHMOTCQRCRERRVEKEKKRKKOYRVE- 167	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Db	23	LCVTVANYDQEDETEPVPQGPQRGRQGEKEKRRH----GEWPSHKEAQPGRERR 75	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Oy	168	QREDDEKEYENKEEDNKRQDQQPQEYEDCRRCEQOEPQYQOCCRRCRQQRHGG 227	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Db	76	ETSEEEFVDEEWRGSQRHEDPEEAR - RYRAEERERRRQWE----- 117	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Oy	228	DLINPQRGGSERVESGEEKQSD - -NEYFEDRSLSRFRFEEGHISLNFYGRSKLLRA 285	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Db	118	-----GEEKEGSSKQERRNPFLFKNSKRFKLFENHGRFLRQLFDKRSDFLEN 167	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Oy	286	LKNYRLVLLLEANPNAFVLPHTDADAILLYGGRGALKMHRDNRSYNRCGYVIRPA 345	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Db	168	LQNYRVEYRAKPTFLPQHIDDLTFLVSGRAILTVLSPDRNSYNERGDTKLPA 227	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Oy	346	GTFYFLINRDRNNRLLTAKFLQTISPGQKPFKQGPQKQPEPYLSTFSEBILAEALNTQ 405	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Db	228	GFTSYLNLQDDEEDLRVUDLIS-SVNRPGKVSFGLSKSN - QYLRGFSKNIASLNTK 285	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Oy	406	AERLRLVVL-----GQORE-----GVTISASSEQIRLTDSESSRRWHIRGGESSRQPYLNENKRP 451	QY	452 RGPYLNFLNKRPLYSNKQGOAYEVKPE-DYRLQDMDSVFLVIANITQGSMGPENTRSTK 510
Oy	1	;	;	;

QY	307	TFNSQYGRITTEVGPDDDEKSMWORLNLMTFTNITORMSTHYNSHAKWVMDGRHL	Db
QY	522	EMACPHLSRGHGRGSKRHEEDEVYQVQARLKSREATIVPVGHPWVVFSSGNEL 581	Db
Db	367	QISCPhMSSRSRDK-----HDSSPSYHRSADLKGPMVWPGHPFTVLSKNEKL 420	Qy
QY	582	LEAFGNAQNHENFLAGRERVLQQEPQAMELAFARPKVEELNSQDSIIFCR 641	Db
Db	421	ITCFEVNVRDNKKFTAGKD-NIVSSLDNVAKELAFNVPSEMVNGVF-ERKESLFFPFEL 478	Qy
QY	642	QHQQSSRS 650	Db
Db	479	PSEERERRA 487	
RESULT	13		
049927			
ID	049927;	PRELIMINARY;	PRT;
AC	049927;	01-JUN-1998 (TREMBLrel. 06, Created)	483 AA.
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	P54 PROTEIN.		
GN	P54.		
OS	Pisum sativum (garden pea).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;		
OC	Rafales; Fabaceae; Papilionoideae; Pisum.		
NCBI_TAXID	3888;		
[1]			
RA	Castillo J., Marquez J.A., Franco L., Ballestar E., Rodrigo M.I.;		
RL	Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; X11207; CAA72050.1; -.		
DR	HSSP; P50477; ICAU.		
DR	MENDEL; 28319; Pisaa3005; 28319.		
DR	INTERPRO; IPR000005; -.		
DR	INTERPRO; IPR001113; -.		
DR	PFAM; PF00546; Seedsstore_7s; 1.		
DR	PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.		
DR	PRODOM; P0081059; -; 1.		
DR	SEQUENCE; 483 AA; 54662 MW; 8127BDAAA0178F3D CRC64;		
RESULT	14		
040873			
ID	040873	PRELIMINARY;	PRT;
AC	040873;	04-Nov-1995 (TREMBLrel. 01, Created)	448 AA.
DT	01-NOV-1995 (TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	VICTIN-LIKE STORAGE PROTEIN.		
OS	Picea glauca (white spruce).		
OC	Congiferopsida; Coniferales; Pinaceae; Picea.		
OX	NCBI_TAXID=3330;		
RN			
RP			
RC			
STRAIN			
TISSUE			
EMBRYO			
RX			
MEDLINE			
RA			
RT	"victin"-like seed storage proteins in the gymnosperm interior spruce (Picea glauca/engelmannii);		
RT	Plant Mol. Biol. 20:315-322(1992).		
RL			
DR	EMBL; X63191; CAA44873.1; -.		
DR	HSSP; P02453; ZPHL.		
DR	MENDEL; 12115; PIC9; 1188; 12115.		
DR	INTERPRO; IPR00113; -.		
DR	PFAM; PF00546; Seedsstore_7s; 1.		
DR	PRODOM; P0081059; -; 1.		
KW	Seed storage protein,		
SQ	SEQUENCE 448 AA; 50200 MW; 467AE5BA12E6D157 CRC64;		
Query Match	21.8%	Score 770.5; DB 10; Length 483;	
Best Local Similarity	31.6%	Pred. No. 4.9e-48;	
Matches	163;	Conservative 113; Mismatches 169; Indels 71; Gaps 12;	
Qy	135	RHETERPHMOCQQRERRYERKEKKQKRKEQQREDEDEYEREEFMEEDNKRDPOQREY 194	Db
Db	28	RKEKDP-ELTTCKDQD-----MQRQDEEDK ----- 53	Qy
Qy	195	EDCRRCEQQEPRQQYOCQRCREOORHQGRGGDLINPQRGSGRYEGEEQKQSDNPYVF 254	Db
Db	54	RICMERD----DVIKKQEROKEH-----EEEEEQEDEDENPYVF 93	Qy
Qy	255	DERSLSTRFRTEEGHISVLENFYGRSKLLRAKKNYRVLLEANPNAFVPLTHADAILL 314	Db
Db	94	EDNDEFTIKDVKGRVLILKNEKSKLKNNTGGLAVLETKANAFLSPHYDSEALLF 153	Qy
Qy	315	VTGGRCALKMTHDRNRSYVNEJCGDVTIRPAGTFYLNDRNNEERIAKFE---LQPTST 371	Db
Db	154	NIKGRGIGIYGWLAEDRTERFNLEEGDIMRVPAFTPMVLFVNDRNEKLUIAFHMPSSGA 213	Qy
Qy	372	PGQYKEFPAGQONPPEYLFSKESKELEAINTAOBRLRGVQOREGVITASQEOIRE 431	Db
Db	214	PVNLERPFESAGRKPESVLNTESSKVLQALKSSKGELETVLDOKGRIFKEKEDVYR 273	Qy
Db	432	LTRDDESESRVHIRROGEESRGPYNLFNKKRPLYSNKYQGAEVVKPEDYRQ LQDMDSVFS 490	Db
Db	274	LAPKKS---LMPP---GGPFKSPPNFNSNIPAFSNKFGSLFEVGPGSOEKLEGNLMLT 327	Qy
Qy	524	ACPHSGRGRGGRGSKRHEEDEVYQVQARLKSREATIVPVGHPWVVFSSGNELLF 583	Db
Db	323	ACPHL-GQHW---SSPRERGDDQDITVORWAKLRTGGSVYIPAGHPIETASTNRLQL 379	Qy
Qy	584	AFGNAQNHENFLAGRERVLQQTEPQAMELAFLAFAAPR-KEVEEFLNSQDSIIFPGPRO 642	

